

SEQUENCE LISTING

<110> Meyers, Rachel
MacBeth, Kyle
Tsai, Fong-Ying

<120> 8797, A NOVEL HUMAN
GALACTOSYLTRANSFERASE AND USES THEREOF

<130> MNI-188

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<151> 2000-08-31

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Met Arg Met Leu Val Ser
1 5

ggc aga aga gtc aaa aaa tgg cag tta att att cag tta ttt gct act 524
Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr
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Cys Phe Leu Ala Ser Leu Met Phe Phe Trp Glu Pro Ile Asp Asn His
25 30 35

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Ile Val Ser His Met Lys Ser Tyr Ser Tyr Arg Tyr Leu Ile Asn Ser
40 45 50

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Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu Lys His Thr Ser Ala Gly
55 60 65 70

cct cgc tac caa tac ttg att aac cac aag gaa aag tgt caa gct caa 716
Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys Glu Lys Cys Gln Ala Gln
75 80 85

gac gtc ctc ctt tta ctg ttt gta aaa act gct cct gaa aac tat gat Asp Val Leu Leu Leu Phe Val Lys Thr Ala Pro Glu Asn Tyr Asp	90	95	100	764	
cga cgt tcc gga att aga agg acg tgg ggc aat gaa aat tat gtt cgg Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg	105	110	115	812	
tct cag ctg aat gcc aac atc aaa act ctg ttt gcc tta gga act cct Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro	120	125	130	860	
aat cca ctg gag gga gaa gaa cta caa aga aaa ctg gct tgg gaa gat Asn Pro Leu Glu Gly Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp	135	140	145	908	
caa agg tac aat gat ata att cag caa gac ttt gtt gat tct ttc tac Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr	155	160	165	956	
aat ctt act ctg aaa tta ctt atg cag ttc agt tgg gca aat acc tat Asn Leu Thr Leu Lys Leu Leu Met Gln Phe Ser Trp Ala Asn Thr Tyr	170	175	180	1004	
tgt cca cat gcc aaa ttt ctt atg act gct gat gat gac ata ttt att Cys Pro His Ala Lys Phe Leu Met Thr Ala Asp Asp Asp Ile Phe Ile	185	190	195	1052	
cac atg cca aat ctg att gag tac ctt caa agt tta gaa caa att ggt His Met Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly	200	205	210	1100	
gtt caa gac ttt tgg att ggt cgt gtt cat cgt ggt gcc cct ccc att Val Gln Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile	215	220	225	230	1148
aga gat aaa agc agc aaa tac tac gtg tcc tat gaa atg tac cag tgg Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser Tyr Glu Met Tyr Gln Trp	235	240	245	1196	
cca gct tac cct gac tac aca gcc gga gct gcc tat gta atc tcc ggt Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly	250	255	260	1244	
gat gta gct gcc aaa gtc tat gag gca tca cag aca cta aat tca agt Asp Val Ala Ala Lys Val Tyr Glu Ala Ser Gln Thr Leu Asn Ser Ser	265	270	275	1292	
ctt tac ata gac gat gtg ttc atg ggc ctc tgt gcc aat aaa ata ggg Leu Tyr Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly	280	285	290	1340	
ata gta ccg cag gac cat gtg ttt tct gga gag ggt aaa act cct Ile Val Pro Gln Asp His Val Phe Ser Gly Glu Gly Lys Thr Pro	295	300	305	1388	
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Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val Asp Thr Tyr Pro Cys Arg	
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Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
35 40 45

Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
50 55 60

Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65 70 75 80

Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr
85 90 95

Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly
100 105 110

Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
115 120 125

Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Leu Gln Arg
130 135 140

Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145 150 155 160

Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
165 170 175

Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
180 185 190

Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln
195 200 205

Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
210 215 220

Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225 230 235 240

Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
245 250 255

Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser
260 265 270

Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
275 280 285

Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
290 295 300

Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met
305 310 315 320

Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala
325 330 335

Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
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Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
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Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
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att cag tta ttt gct act tgt ttt tta gcg agc ctc atg ttt ttt tgg				96
Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp				
20 25 30				
gaa cca atc gat aat cac att gtg agc cat atg aag tca tat tct tac				144
Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr				
35 40 45				
aga tac ctc ata aat agc tat gac ttt gtg aat gat acc ctg tct ctt				192
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu				
50 55 60				
aag cac acc tca gcg ggg cct cgc tac caa tac ttg att aac cac aag				240
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys				
65 70 75 80				
gaa aag tgt caa gct caa gac gtc ctc ctt tta ctg ttt gta aaa act				288
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Phe Val Lys Thr				
85 90 95				
gct cct gaa aac tat gat cga cgt tcc gga att aga agg acg tgg ggc				336
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly				
100 105 110				
aat gaa aat tat gtt cgg tct cag ctg aat gcc aac atc aaa act ctg				384
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu				
115 120 125				
ttt gcc tta gga act cct aat cca ctg gag gga gaa gaa cta caa aga				432
Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Leu Gln Arg				
130 135 140				
aaa ctg gct tgg gaa gat caa agg tac aat gat ata att cag caa gac				480
Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp				
145 150 155 160				
ttt gtt gat tct ttc tac aat ctt act ctg aaa tta ctt atg cag ttc				528
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe				
165 170 175				
agt tgg gca aat acc tat tgt cca cat gcc aaa ttt ctt atg act gct				576
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala				
180 185 190				
gat gat gac ata ttt att cac atg cca aat ctg att gag tac ctt caa				624
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln				
195 200 205				
agt tta gaa caa att ggt gtt caa gac ttt tgg att ggt cgt gtt cat				672
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His				
210 215 220				

cgt ggt gcc cct ccc att aga gat aaa agc agc aaa tac tac gtg tcc		720
Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser		
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Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala		
245	250	255
gcc tat gta atc tcc ggt gat gta gct gcc aaa gtc tat gag gca tca		816
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser		
260	265	270
cag aca cta aat tca agt ctt tac ata gac gat gtg ttc atg ggc ctc		864
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu		
275	280	285
tgt gcc aat aaa ata ggg ata gta ccg cag gac cat gtg ttt ttt tct		912
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser		
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Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met		
305	310	315
320		
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Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala		
325	330	335
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Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile		
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Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val		
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Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile		
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